

RAW SEQUENCE LISTING

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Application Serial Number: 09/613,170
Source: IFW16
Date Processed by STIC: 5/9/05

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IFW16

RAW SEQUENCE LISTING

DATE: 05/09/2005

PATENT APPLICATION: US/09/613,170

TIME: 16:20:18

Input Set : N:\CrF3\RULE60\09613170.raw

Output Set: N:\CRF4\05092005\I613170.raw

SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
5     (i) APPLICANT: Ueda, Tetsufumi
6           Ozkan, Eric D.
8     (ii) TITLE OF INVENTION: Compositions And Methods For The
9           Inhibition Of Neurotransmitter Uptake Of Synaptic
Vesicles
11    (iii) NUMBER OF SEQUENCES: 6
13    (iv) CORRESPONDENCE ADDRESS:
14          (A) ADDRESSEE: Medlen & Carroll, LLP
15          (B) STREET: 220 Montgomery Street, Suite 2200
16          (C) CITY: San Francisco
17          (D) STATE: California
18          (E) COUNTRY: United States of America
19          (F) ZIP: 94104
21    (v) COMPUTER READABLE FORM:
22          (A) MEDIUM TYPE: Floppy disk
23          (B) COMPUTER: IBM PC compatible
24          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27    (vi) CURRENT APPLICATION DATA:
C--> 28          (A) APPLICATION NUMBER: US/09/613,170
C--> 29          (B) FILING DATE: 10-Jul-2000
30          (C) CLASSIFICATION: 514
32    (vii) PRIOR APPLICATION DATA:
33          (A) APPLICATION NUMBER: US/08/840,006
34          (B) FILING DATE: 15-APR-1997
36    (viii) ATTORNEY/AGENT INFORMATION:
37          (A) NAME: Carroll, Peter G.
38          (B) REGISTRATION NUMBER: 32,837
39          (C) REFERENCE/DOCKET NUMBER: UM-02786
41    (ix) TELECOMMUNICATION INFORMATION:
42          (A) TELEPHONE: (415) 705-8410
43          (B) TELEFAX: (415) 397-8338
46 (2) INFORMATION FOR SEQ ID NO: 1:
48     (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 10 amino acids
50          (B) TYPE: amino acid
51          (C) STRANDEDNESS: Not Relevant
52          (D) TOPOLOGY: linear
54     (ii) MOLECULE TYPE: peptide
59     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61     Glu Ala Ala Leu Thr Ser Glu Glu Val Gly
62     1             5             10

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64 (2) INFORMATION FOR SEQ ID NO: 2:

66 (i) SEQUENCE CHARACTERISTICS:

67 (A) LENGTH: 5 amino acids

68 (B) TYPE: amino acid

69 (C) STRANDEDNESS: Not Relevant

70 (D) TOPOLOGY: linear

72 (ii) MOLECULE TYPE: peptide

77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

79 Tyr His Arg Phe Lys

80 1 5

82 (2) INFORMATION FOR SEQ ID NO: 3:

84 (i) SEQUENCE CHARACTERISTICS:

85 (A) LENGTH: 10 amino acids

86 (B) TYPE: amino acid

87 (C) STRANDEDNESS: Not Relevant

88 (D) TOPOLOGY: linear

90 (ii) MOLECULE TYPE: peptide

95 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

97 Tyr His Arg Phe Lys Glu Leu Ser Thr Leu

98 1 5 10

100 (2) INFORMATION FOR SEQ ID NO: 4:

102 (i) SEQUENCE CHARACTERISTICS:

103 (A) LENGTH: 20 amino acids

104 (B) TYPE: amino acid

105 (C) STRANDEDNESS: Not Relevant

106 (D) TOPOLOGY: linear

108 (ii) MOLECULE TYPE: peptide

113 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

115 Tyr His Arg Phe Lys Glu Leu Ser Thr Leu Arg Arg Gln Lys Leu Glu

116 1 5 10 15

118 Asp Ser Tyr Arg

119 20

121 (2) INFORMATION FOR SEQ ID NO: 5:

123 (i) SEQUENCE CHARACTERISTICS:

124 (A) LENGTH: 1200 amino acids

125 (B) TYPE: amino acid

126 (C) STRANDEDNESS: Not Relevant

127 (D) TOPOLOGY: linear

129 (ii) MOLECULE TYPE: peptide

134 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

136 Met Asp Pro Ser Gly Val Lys Val Leu Glu Thr Ala Glu Asp Ile Gln

137 1 5 10 15

139 Glu Arg Arg Gln Gln Val Leu Asp Arg Tyr His Arg Phe Lys Glu Leu

140 20 25 30

142 Ser Thr Leu Arg Arg Gln Lys Leu Glu Asp Ser Tyr Arg Phe Gln Phe

143 35 40 45

145 Phe Gln Arg Asp Ala Glu Glu Leu Glu Lys Trp Ile Gln Glu Lys Leu

146 50 55 60

148 Gln Ile Ala Ser Asp Glu Asn Tyr Lys Asp Pro Thr Asn Leu Gln Gly

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149	65		70		75		80
151	Lys	Leu	Gln	Lys	His	Gln	Ala
152				85			90
154	Gly	Ala	Ile	Val	Lys	Leu	Asp
155			100			105	
157	Gly	His	Phe	Ala	Ser	Glu	Thr
158		115				120	
160	Arg	Gln	Trp	Glu	Leu	Leu	Leu
161		130				135	
163	Leu	Leu	Gln	Ala	Gln	Asn	Leu
164		145			150		155
166	Val	Met	Asp	Trp	Ile	Asn	Asp
167			165			170	
169	Leu	Gly	Gln	Asp	Leu	Glu	His
170			180			185	
172	Glu	Phe	Gln	Thr	Asp	Met	Ala
173		195				200	
175	Asn	Gln	Phe	Ala	Ala	Lys	Leu
176		210				215	
178	Leu	Ile	Lys	Thr	Lys	Gln	Asp
179		225			230		235
181	Lys	Gly	Leu	Ala	Leu	Gln	Arg
182			245			250	
184	Val	Gln	Arg	Phe	Asn	Arg	Asp
185		260				265	
187	Glu	Lys	Glu	Gln	Leu	Met	Ala
188		275				280	
190	Ser	Val	Gln	Ala	Leu	Leu	Arg
191		290				295	
193	Ala	Ala	Leu	Glu	Asp	Lys	Val
194		305				310	
196	Leu	Gln	Gln	Ser	His	Pro	Leu
197			325			330	
199	Glu	Glu	Leu	Ile	Thr	Asn	Trp
200			340			345	
202	Arg	His	Ala	Arg	Leu	Asn	Asp
203		355				360	
205	Asp	Phe	Arg	Asp	Leu	Thr	Ser
206		370				375	
208	Asn	Ala	Asp	Glu	Leu	Ala	Ser
209		385				390	
211	Asp	Arg	His	Gln	Glu	His	Lys
212			405			410	
214	Phe	Lys	Ser	Ala	Asp	Glu	Ser
215			420			425	
217	Tyr	Ala	Ser	Asp	Glu	Val	Arg
218		435				440	
220	Arg	Ala	Ala	Leu	Leu	Glu	Leu
221		450				455	

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223   Gln Cys Met Asp Leu Gln Leu Phe Tyr Arg Asp Thr Glu Gln Val Asp
224   465                               470                               475                               480
226   Asn Trp Met Ser Lys Gln Glu Ala Phe Leu Leu Asn Glu Asp Leu Gly
227                               485                               490                               495
229   Asp Phe Leu Asp Ser Val Glu Ala Leu Lys Lys His Glu Asp Phe
230                               500                               505                               510
232   Glu Lys Ser Leu Ser Ala Gln Glu Lys Ile Thr Ala Leu Asp Glu
233                               515                               520                               525
235   Phe Ala Thr Lys Leu Ile Gln Asn Asn His Tyr Ala Met Glu Asp Val
236                               530                               535                               540
238   Ala Thr Arg Arg Asp Ala Leu Leu Ser Arg Arg Asn Ala Leu His Glu
239   545                               550                               555                               560
241   Arg Ala Met Arg Arg Arg Ala Gln Leu Ala Asp Ser Phe His Leu Gln
242                               565                               570                               575
244   Gln Phe Phe Arg Asp Ser Asp Glu Leu Lys Ser Trp Val Asn Glu Lys
245                               580                               585                               590
247   Met Lys Thr Ala Thr Asp Glu Ala Tyr Lys Asp Pro Ser Asn Leu Gln
248                               595                               600                               605
250   Gly Lys Val Gln Lys His Gln Ala Phe Glu Ala Glu Leu Ser Ala Asn
251   610                               615                               620
253   Gln Ser Arg Ile Asp Ala Leu Glu Lys Ala Gly Gln Lys Leu Ile Asp
254   625                               630                               635                               640
256   Val Asn His Tyr Ala Lys Asp Glu Val Ala Ala Arg Met Asn Glu Val
257                               645                               650                               655
259   Ile Ser Leu Trp Lys Lys Leu Leu Glu Ala Thr Glu Leu Lys Gly Ile
260                               660                               665                               670
262   Lys Leu Arg Glu Ala Asn Gln Gln Gln Gln Phe Asn Arg Asn Val Glu
263   675                               680                               685
265   Asp Ile Glu Leu Trp Leu Tyr Glu Val Glu Gly His Leu Ala Ser Asp
266   690                               695                               700
268   Asp Tyr Gly Lys Asp Leu Thr Asn Val Gln Asn Leu Gln Lys Lys His
269   705                               710                               715                               720
271   Ala Leu Leu Glu Ala Asp Val Ala Ala His Gln Asp Arg Ile Asp Gly
272                               725                               730                               735
274   Val Thr Ile Gln Ala Arg Gln Phe Gln Asp Ala Gly His Phe Asp Ala
275   740                               745                               750
277   Glu Asn Ile Lys Lys Lys Gln Glu Ala Leu Val Ala Arg Tyr Glu Ala
278   755                               760                               765
280   Leu Lys Glu Pro Met Val Ala Arg Lys Gln Lys Leu Ala Asp Ser Leu
281   770                               775                               780
283   Arg Leu Gln Gln Leu Phe Arg Asp Val Glu Asp Glu Glu Thr Trp Ile
284   785                               790                               795                               800
286   Arg Glu Lys Glu Pro Ile Ala Ala Ser Thr Asn Arg Gly Lys Asp Leu
287                               805                               810                               815
289   Ile Gly Val Gln Asn Leu Leu Lys Lys His Gln Ala Leu Gln Ala Glu
290   820                               825                               830
292   Ile Ala Gly His Glu Pro Arg Ile Lys Ala Val Thr Gln Lys Gly Asn
293   835                               840                               845
295   Ala Met Val Glu Glu Gly His Phe Ala Ala Glu Asp Val Lys Ala Lys

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296      850      855      860
298  Leu His Glu Leu Asn Gln Lys Trp Glu Ala Leu Lys Ala Lys Ala Ser
299      865      870      875      880
301  Gln Arg Arg Gln Asp Leu Glu Asp Ser Leu Gln Ala Gln Gln Tyr Phe
302      885      890      895
304  Ala Asp Ala Asn Glu Ala Glu Ser Trp Met Arg Glu Lys Glu Pro Ile
305      900      905      910
307  Val Gly Ser Thr Asp Tyr Gly Lys Asp Glu Asp Ser Ala Glu Ala Leu
308      915      920      925
310  Leu Lys Lys His Glu Ala Leu Met Ser Asp Leu Ser Ala Tyr Gly Ser
311      930      935      940
313  Ser Ile Gln Ala Leu Arg Glu Gln Ala Gln Ser Cys Arg Gln Gln Val
314      945      950      955      960
316  Ala Pro Thr Asp Asp Glu Thr Gly Lys Glu Leu Val Leu Ala Leu Tyr
317      965      970      975
319  Asp Tyr Gln Glu Lys Ser Pro Arg Glu Val Thr Met Lys Lys Gly Asp
320      980      985      990
322  Ile Leu Thr Leu Leu Asn Ser Thr Asn Lys Asp Trp Trp Lys Val Glu
323      995      1000      1005
325  Val Asn Asp Arg Gln Gly Phe Val Pro Ala Ala Tyr Val Lys Lys Leu
326      1010      1015      1020
328  Asp Pro Ala Gln Ser Ala Ser Arg Glu Asn Leu Leu Glu Glu Gln Gly
329      1025      1030      1035      1040
331  Ser Ile Ala Leu Arg Gln Glu Gln Ile Asp Asn Gln Thr Arg Ile Thr
332      1045      1050      1055
334  Lys Glu Ala Gly Ser Val Ser Leu Arg Met Lys Gln Val Glu Glu Leu
335      1060      1065      1070
337  Tyr His Ser Leu Leu Glu Leu Gly Glu Lys Arg Lys Gly Met Leu Glu
338      1075      1080      1085
340  Lys Ser Cys Lys Lys Phe Met Leu Phe Arg Glu Ala Asn Glu Leu Gln
341      1090      1095      1100
343  Gln Trp Ile Asn Glu Lys Glu Ala Ala Leu Thr Ser Glu Glu Val Gly
344      1105      1110      1115      1120
346  Ala Asp Leu Glu Gln Val Glu Val Leu Gln Lys Lys Phe Asp Asp Phe
347      1125      1130      1135
349  Gln Lys Asp Leu Lys Ala Asn Glu Ser Arg Leu Lys Asp Ile Asn Lys
350      1140      1145      1150
352  Val Ala Glu Asp Leu Glu Ser Glu Gly Leu Met Ala Glu Glu Val Gln
353      1155      1160      1165
355  Ala Val Gln Gln Gln Glu Val Tyr Gly Met Met Pro Arg Asp Glu Thr
356      1170      1175      1180
358  Asp Ser Lys Thr Ala Ser Pro Trp Lys Ser Ala Arg Leu Met Val His
359      1185      1190      1195      1200

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362 (2) INFORMATION FOR SEQ ID NO: 6:

364 (i) SEQUENCE CHARACTERISTICS:

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365 (A) LENGTH: 1151 amino acids
366 (B) TYPE: amino acid
367 (C) STRANDEDNESS: Not Relevant
368 (D) TOPOLOGY: linear

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/613,170

DATE: 05/09/2005

TIME: 16:20:19

Input Set : N:\Crf3\RULE60\09613170.raw

Output Set: N:\CRF4\05092005\I613170.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]